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(without alignments) 5752.514 Million cell updates/sec
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                                                                                                                                September 11, 2003, 19:05:45 ; Search time 229 Seconds
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                   2552756 seqs, 1349719017 residues
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Maximum Match 100%
Listing first 45 summaries
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/SIDSI/gcgdata/geneseq/geneseqn-embl/NN2002.DAT:*
/SIDSI/gcgdata/geneseq/geneseqn-embl/NN2002.DAT:* N_Geneseq_19Jun03:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	Corn tassel-derive	674 bp region of p	Partial sequence o	Pseudorabies virus	Human nervous syst	Aujeszky's disease	Arabidopsis thalia	Streptomyces fradi
		ID	ABL71419	AAA61490	AAN50036	AAQ03259	ABA17777	AAV49291	ABL93562	AAQ52638
		DB	24	21	9	11	22	19	24	14
		Match Length DB ID	273	674	2796	4897	11396	2742	465	2064
ф	Query	Match	9.1	8.4	8.4	8.4	8.2	8.1	7.8	7.4
		Score	44.6	41	41	41	40	39.4	38	36.2
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) ر	-, -	9 0		25360	, ,	AAE88314	4900
י נ	12	3.0		29736	22	31	DNA
o c		ď		3283	22	AAS63231	A encoding Th
) C			•	1473	2 00	AAT64548	NADP-specific glut
ט כ		. n		1473	24	ABK51026	
U				1506	24	ABK51025	encoding
O		5		1969	18	AAT64531	Glutamate dehydrog
O		5		1969	24	ABK51009	
υ		5.	•	2096	18	AAT64543	NADP-specific glut
ပ		5.	•	2096	24	ABK51021	
O		٠.		2099	18	AAT64530	NADP-specific glut
U		س		2099	24	ABK51008	
O		ر. د	٠	2137	8 -	AAT64542	NADP-specific glut
o c	4. c	35.0 25.0	- r	213/	4 c	ABK51020 aam64529	NADP-glutamate den NaDD-specific glut
ט ט				2140	24	ABK51007	
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υ		5.		35134	23	ABL50990	Thermus caldophilu
O		5		417	24	ABS68109	B-domain-deleted-F
O		ъ.		926	24	ABL89975	Human polynucleoti
υ		ū.	۳.	80557	24	ABX09142	Mycobacterium tube
ပ		٠. ا	m.	4403765	22	AA199683	
U		'n	m,	4411529	22	AA199682	Mycobacterium tube
ပ		ς,	7	3193	20	AAX19252	ydrogue
ပ	3.5	35	? (428	21	AAC56164	
U (ກຸ	7 -	50T	2 2	ABX64419	Human gene trapped
ט כ		34.6		1796	2 7	AAS/880/ ABS51676	DNA encoding nover
0		. 4	: -:	2123	21	AAC60997	Human vesicle asso
U		4	-:	2452	22	AAH17574	Human cDNA sequenc
O		4.	٦.	4799	21	AAC76258	Human ORFX ORF1813
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O		₹	0	2940	21	AAA36699	sed
O		34.4	7.0	3106	27	AAA36696	ised F-RSV/H
ย		`. ₹	?	3540	7.7	787	
						ALIGNMENTS	
RESULT ABL714	RESULT 1						
a a s	ABL71419	419	standard;	i; cDNA;	273	BP.	
¥C H	ABL71419	419;			٠		
TO	14-MAY	Y-2002	(first	st entry	2		
S E S	Corn	Corn tassel-derived	leriv		nucle	polynucleotide (cdps) SEQ ID NO:793	793.
X X	Corn		ssel	-derive	00	corn tassel-derived polynucleotide; cdps; hyb;	cdps: hybrid breeding: CDPs:
X	inher		char	acterist	Lic;	growth; development;	ance;

Innerlance, characteristic, growin, development, disease res environmental adaptability; quality; yield; molecular marker; multigene trait; plant breeding; corn tassel; gene; ss.

Zea mays

US2001051335-A1.

13-DEC-2001.

99US-0294093 16-APR-1999;

98US-082567P. 21-APR-1998;

(LALG/) LALGUDI R V. (ITOL/) ITO L Y. (SHER/) SHERMAN B K.

Sherman BK; Lalgudi RV, Ito LY,

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RESULT 3
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                                                                                                                                polynucleotide acquence (cgs) comprising a nucleic acid sequence selected from those given in AB170627 to AB176833. The cdps sequence selected from those given in AB170627 to AB176833. The cdps sequences can be used for determining altered gene expression, to recover can be used for determining altered gene expression, to recover regulatory elements and to follow inheritance of desirable characteristics through hybrid breeding programs. (I) are also useful in the evaluation, and alteration of desirance, environmental adaptability, quality and yield, and am molecular markers for studying inheritance of multigene traits in a plant breeding program. (I) can be used to produce a tassel-specific profile of gene transcription, a transformation vectors, to express a polypeptide, to identify, isolate or extend identical or related corn tassel nucleic acid sequences from DNA is a query sequences to determine hybridisation, and to identify the presence of an advort nor Northern hybridisation, and to identify between two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             291 CGGGGGGTGCCACCCGGCAGGTGTTGTGGGACTGGCAGTGGCAGCACTTGTGGCCCGCCA 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             determining altered gene expression, to recover regulatory elements and to follow inheritance of desirable characteristics through hybrid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pseudorabies virus gII gene; glycoprotein gII; latent virus detection; pig; Sus scrofa; diagnosis; nested PCR amplification; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                351 CGCCGGAGAACCTGCGTCGTGTCCTGCAGTCGTTGCACGACCCATCCCTT 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          134 CGTGAAAGTTCACCTCTGAGACCTTGTTGCAATCGTTGCAAAGCACCCCAAATCTT 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                         The present sequence describes a purified corn tassel-derived
                                                                                                                                                                                                                                                                                                                                                                                                                                     9.1%; Score 44.6; DB 24; Length 273; 61.7%; Pred. No. 0.0017;
                           purified corn tassel-derived polynucleotide useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              674 bp region of pseudorabies virus glycoprotein gII gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 273 BP; 83 A; 69 C; 61 G; 60 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 0.0017;
0; Mismatches 44
                                                                                              Claim 1; SEQ ID 793; 201pp; English.
                                                                                                                                                                                                                                                                                                                                                                                  (or more) nucleic acid sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAA61490 standard; DNA; 674 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-0069811.
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                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
Best Local Similarity والمرابع المرابع مرابع 71; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-410853/35.
WPI; 2002-163647/21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pseudorabies virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (KLAN/) KLANN R C.
                                                                    breeding programs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Klann RC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAA61490;
                           Novel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 2
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The invention relates to a method of detecting pseudorables virus in samples. The method comprises performing a nested PCR to amplify a target nucleotide sequence in a purified sample nucleot acid mixture. In the first stage of the nested PCR, a 674 bp region of the pseudorables gir gene (AAA61490), which encodes a glycoprotein essential for viral teplication is amplified. An aliquot of the first stage PCR mixture is then removed and a second target region contained within the 674 bp region is amplified in the second stage of the nested PCR. The first and second stage PCR reaction mixtures are analysed to detect the first and second stage PCR reaction mixtures are analysed to detect the first and second stage PCR products which will indicate the presence of the virus in the sample. The nested PCR primers are selected from the 674 bp region. The outer, first stage PCR primers are AAA61491 (upper primer) and either AAA61492 or AAA62493 (lower primers), and the inner, second stage PCR primers are one selected from AAA61494-A61496 (upper primers) and one selected from AAA61494-A61496 (upper primers) being infected with the virus. The pseudorabies virus causes a disease which is generally fatal to young pigs. Those which survive become reactivated and spread to other susceptible animals. The method allows for greater detection of the virus in the latent form when disease are virus in tonsillar tissues, before visible signs of the virus of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    349 CACGCCGGAGAAGACCTGCGTGTGTCCTGCAGTCGTTGCACACGACCCATCCTTTCC 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 evident or after visible signs of the disease have dissipated. The present sequence represents the 674 bp region of the pseudorables virus gII gene which is amplified in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               409 CGTGTACAAGTAGCTTGCCTCCATCTGCGTCGAGGGCCTTGAAGAACTTGTCCATGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
Detecting for the presence of Pseudorabies virus in a sample by performing nested polymerase chain reaction comprising two stage
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.4%; Score 41; DB 21; Length 674; 56.2%; Pred. No. 0.032;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 674 BP; 126 A; 253 C; 202 G; 93 T; 0 other;
                                                                           amplification of a targeted nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                       claim 1c i; Column 13-14; 16pp; English.
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136..141
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262..2796
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misc_difference 2796
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Matches 77; Conservative
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07-SEP-1991
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Lukacs N,

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349 CACGCCGGAGAAGACCTGCGTCGTGTCCTGCAGTCGTTGCACACGACCCATCCCTTTCC 408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1810 CAGGCCGTAGAAGGGGGACATGTACACGATGTCCCCCGTGGACAGGGCGGAAGGAGTCGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   409 CGTGTACAAGTAGCTTGCCTCCATCTCTGCGTCGAGGGCCTTGAAGAACTTGTCCATGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 8.4%; Score 41; DB 11; Length 4897; Best Local Similarity 56.2%; Pred. No. 0.074; Matches 77; Conservative 0; Mismatches 60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human nervous system related polynucleotide SEQ ID NO 10108.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4897 BP; 594 A; 2052 C; 1495 G; 756 T; 0 other;
                                                                                                                                                                                                                                                            Immunogenic polypeptide of pseudo-rabies virus -
for use in mammalian vaccine against Aujeszky's disease.
                                                                                                                                                                                                                                                                                                                                    The polypeptide may be used as a vaccine to provide mammals, e.g. pigs, with resistance against Aujeszky's
                                                                                                                                                                                                                                                                                                                                                                              (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct PI field.)
 /note="gII glycoprotein"
                                                                                                                                                                                        Simon AR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABA1777/c
ID ABA17777 standard; DNA; 11396 BP.
                                                                                                                                                                                                                                                                                                        Disclosure; Fig 1; 21pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1690 GTAGAAGCCCGCGCGCC 1674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             469 GAAGATGGGCGTGGCGC 485
                                                                                                                                                                                       Schreurs CS, Mettenleit TC,
                                                                                    89EP-0201887
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NOBEL NV.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1200 caggeceragaegegereargracacaarerececegegaeagegegaegergra 1141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        349 CACGCCGGAGAAGACCTGCGTCGTGTCCCTGCAGTCGTTGCACGACCCATCCCTTTCC 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      409 CGTGTACAAGTAGCTTGCCTCCATCTCTGCGTCGAGGGCCTTGAAGAACTTGTCCATGTC 468
                                                                                                                                                                                                                                                                                                                                                                          The inventors claim a recombinant vector comprising a DNA sequence coding for an immunoreactive and antigenic determinant of a Pseudorables virus protein, and a polypeptide having an immunoreactive and antigenic determinant of a Pseudorables virus protein. Vaccines contg. the polypeptide are obtd. economically and in large amts., for use in conferring protection against Pseudorables virus. (Updated on 25-MAR-2003 to correct PD field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
            "approx. 300 bps at the 3' end of this gene are missing"
                                                                                                                                                                                                                                                                                      Prodn. of Pseydorables virus sub-unit vaccines - useful for conferring protection against the virus infections and for diagnosis esp. with sheep sera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 41; DB 6; Length 2796;
Pred. No. 0.058;
0; Mismatches 60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2796 BP; 408 A; 1040 C; 945 G; 403 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pseudorabies virus glycoprotein gII polypeptide.
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2639..3001
/*tag= a
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ID AAQ03259 standard; DNA; 4897 BP.
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                                                                                                                                                                                       (MOLE-) MOLECULAR GENETICS INC
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84US-0598073.
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Local Similarity 56.2%;
nes 77; Conservative
                                                                                                                85EP-0400704
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(first entry)
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/*tag=
/note=
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P-PSDB; AAP50035.
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                                                                                                                                                          09-APR-1984;
                                                                                                                09-APR-1985;
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22-JUL-1990
                                                                                                                                            03-APR-1985;
                                                                                   27-NOV-1985
                                                        EP162738-A
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PR 29-SEP-2000; 2000US-0236370. PR 02-OCT-2000; 2000US-0236802. PR 02-OCT-2000; 2000US-0237037. PR 02-OCT-2000; 2000US-0237038. PR 02-OCT-2000; 2000US-0237039. PR 13-OCT-2000; 2000US-023937. PR 20-OCT-2000; 2000US-023937. PR 20-OCT-2000; 2000US-0241785. PR 20-OCT-2000; 2000US-0241786. PR 20-OCT-2000; 2000US-0241786. PR 20-OCT-2000; 2000US-0241786. PR 20-OCT-2000; 2000US-0241899. PR 20-OCT-2000; 2000US-024189. PR 20-OCT-2000; 2000US-0244677. PR 08-NOV-2000; 2000US-0246677. PR 08-NOV-2000; 2000US-0246677. PR 08-NOV-2000; 2000US-0246677. PR 08-NOV-2000; 2000US-0246677. PR 08-NOV-2000; 2000US-0246611. PR 17-NOV-2000; 2000US-0249229. PR 17-NOV-2000; 2000US-0249211. PR 17-NOV-2000; 2000US-024929. PR 17-NOV-	11-DEC-2000; 05-JAN-2001; (HUMA-) HUMA Rosen CA, B WPI; 2001-54 Nucleic acid
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2000US-01334. 2000US-013965. 2000US-0184664. 2000US-0184664. 2000US-0184664. 2000US-0184664. 2000US-018123. 2000US-018131. 2000US-018131. 2000US-018131. 2000US-0218139. 2000US-0218139. 2000US-0218139. 2000US-0218139. 2000US-0218139. 2000US-0218139. 2000US-0218139. 2000US-0218139. 2000US-0218139. 2000US-02181344. 2000US-02181344. 2000US-02181344. 2000US-02181344. 2000US-02181344. 2000US-02181344. 2000US-02181344. 2000US-02181344. 2000US-02181344. 2000US-02181414. 2000US-02181414. 2000US-02181414. 2000US-02181418. 2000US-02181419. 2000US-02181419. 2000US-02181419. 2000US-02181419. 2000US-02181968. 2000US-02181968. 2000US-02181968. 2000US-02181968. 2000US-02181968. 2000US-02181968. 2000US-02181968. 2000US-02181968. 2000US-02181968.	2000US-0234274 2000US-0234997 2000US-0235484 2000US-0235834 2000US-0235836 2000US-0235836 2000US-0236363 2000US-0236369 2000US-0236369
17 - JAN - 2001; 31 - JAN - 2000; 34 - FEB - 2000; 24 - FEB - 2000; 16 - MAR - 2000; 16 - MAR - 2000; 17 - MAR - 2000; 18 - MAP - 2000; 19 - MAP - 2000; 10 - MAP - 2000; 11 - JUL - 2000; 12 - AUG - 2000; 14 - AUG - 2000; 14 - AUG - 2000; 15 - AUG - 2000; 16 - SEP - 2000; 17 - AUG - 2000; 18 - AUG - 2000; 18 - AUG - 2000; 19 - AUG - 2000; 10 - SEP - 2000; 10 - SEP - 2000; 11 - SEP - 2000; 12 - SEP - 2000; 13 - SEP - 2000; 14 - SEP - 2000; 16 - SEP - 2000; 17 - SEP - 2000; 18 - SEP - 2000; 18 - SEP - 2000; 19 - SEP - 2000; 10 - SEP - 2000; 11 - SEP - 2000; 12 - SEP - 2000; 14 - SEP - 2000; 16 - SEP - 2000; 17 - SEP - 2000; 18 - SEP - 2000; 18 - SEP - 2000; 19 - SEP - 2000; 10 - SEP - 2000; 11 - SEP - 2000; 11 - SEP - 2000; 12 - SEP - 2000; 13 - SEP - 2000; 14 - SEP - 2000; 14 - SEP - 2000; 15 - SEP - 2000; 16 - SEP - 2000; 17 - SEP - 2000; 18 - SEP - 2000; 18 - SEP - 2000; 18 - SEP - 2000; 19 - SEP - 2000; 11 - SEP - 2000; 11 - SEP - 2000; 12 - SEP - 2000; 13 - SEP - 2000; 14 - SEP - 2000; 15 - SEP - 2000; 16 - SEP - 2000; 17 - SEP - 2000; 18 - SEP - 2000; 18 - SEP - 2000; 19 - SEP - 2000; 11 - SEP - 2000; 11 - SEP - 2000; 12 - SEP - 2000; 13 - SEP - 2000; 14 - SEP - 2000; 15 - SEP - 2000; 16 - SEP - 2000; 17 - SEP - 2000; 18 - SEP - 2000; 19 - SEP - 2000; 10 - SEP - 2000; 10 - SEP - 2000; 11 - SEP - 2000; 11 - SEP - 2000; 12 - SEP - 2000; 12 - SEP - 2000; 13 - SEP - 2000; 14 - SEP - 2000; 15 - SEP - 2000; 16 - SEP - 2000; 17 - SEP - 2000; 18 - S	SEP-2000; SEP-2000; SEP-2000; SEP-2000; SEP-2000; SEP-2000; SEP-2000; SEP-2000;

ous system antigen polypeptides,

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10-JUN-2002
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  23-JAN-1998
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                                                                                         The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB1678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, alleragies, autoimmune hamonytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from MIPO at ftp.Wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1199 CCTCCATGGGCGCCCCCATCTTGCCTTCCCCACGCCCCGGACGTGCGTCATCATGAGCG 1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1319 GCAGCGCCAGGCCGCGGGGTCCCGCCTGGCCGCCGCGGTAGGTGGCAGGTTGGCGCCCCG 1260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                279 GCTACGGAAGGACGGGGGGGGCCCCCCGCCAGGTGTTGTGGGGACTGGCAGTGGCAGCACT 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             339 TGTGGCCCGCCACGCCGGAGAAGACCTGCGTGTCCCTGCAGTCGTTGCACACGACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            399 ATCCCTTTCCCGTGTACAAGTAGCTTGCCTCCATCTCTGCGTCGAGGGCCTTGAAGAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
diagnosing and/or treating nervous system
                                                              English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8.2%; Score 40; DB 22; Length 11396; 50.5%; Pred. No. 0.21; Live 0; Mismatches 95; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 11396 BP; 1996 A; 3549 C; 3532 G; 2319 T; 0 other;
                                                   SEQ ID NO 10108; 1701pp + Sequence Listing;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product= "glycoprotein gB"
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1..2742
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ID AAV49291 standard; DNA; 2742 BP.
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Best Local Similarity 50.5%
Matches 97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         459 TGTCCATGTCGA 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag=
useful for preventing, cancers and metastases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          against several pathogens, especially pathogens associated with respiratory and digestive diseases. The pathogens are especially pathogens are especially pathogens are especially portion and especially solutions with an interest of the pathogens are especially portion respiratory and reproductive syndrome virus (PRRSV), hog cholera virus (HCV) and Actinobacillus pleuropneumoniae. The vaccines are preferably composed of polynuclectide sequences encoding 3 antigens, all as part of vectors. This sequence represents the coding region for the Aujeszky's disease virus strain NIA3 glycoprotein 9B. The sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Aujeszky's disease virus strain NIA3 glycoprotein gB. The sequence subcloned into the plasmid pVR1012 to generate plasmid pAB090 for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       349 CACGCCGGAGAAGACCTGCGTGTGTCCCTGCAGTCGTTGCACGACCCATCCCTTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   939 CAGGCCGTAGAAGGGGGACATGTACACAATGTCCCCCGTGGACAGGGCGAAGGAGTCGTA
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                                                                                                                                                                                                                                                                      Multi-valent polynucleotide vaccines against porcine pathogens -
consist of at least 3 plasmids able to express protective antigens
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    invention relates to a multivalent vaccine for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61;
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Pred. No. 0.
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0
                                                                                                                                                                                                                                                                                                                                                                                              Example 8; Fig 2; 63pp; French.
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55.5%;
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96FR-0009338
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Best Local Similarity 55.5
Matches 76; Conservative
                                                                                                                                                                                                                                                                                                                               from specified viruses
                                                                                                                    (INMR ) RHONE MERIEUX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              273 GGCGAGTGTTGTATGATTTGCAGTTTGGGCATTTCTGAGCCACCACCACGTGGTACTGTACCT 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes an Arabidopsis thaliana nucleic acid (I) comprising a sequence capable of hybridising under stringent conditions to a sequence (Si) selected from any one of the 999 sequences given in ABL9336 to ABL9434. (I) have insecticide and fundicide activities, and they can be used as protein expression modulators. (I) can be used in Identifying homologous or related genes, in producing compositions that modulate the expression or function of their encoded proteins, mapping functional regions of the proteins, and in studying associated physiological pathways. (I) can also be used: (1) for the genetic manipulation of cells, particularly plant cells; (2) in screening assays of various plant strains to determine the strains that are best capable of withstanding a particular disease or environmental stress; (3) for the chancing or inhibiting production of a blosynthetic product in a plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (4) as probes in mapping and in diagnosis, in genetic modification and for screening purposes, to generate additional copies of the nucleic acids, to generate ribozymes or antisense oligonucleotides, and as single-stranded DNA probes or as triple-stand forming oligonucleotides; and (5) for generating genetically modified transgenic organisms.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                              function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCGTCGTGTCCCTGCAGTCGTTGCACACGACCCATCCCTTTCCCGTGTACAAGTAGCTTG
                                                                                                                                                                                                                                                                                                             Yu Y;
JP, Haas WD;
                                                                                                                                                                                                                                                                                                                                                                                                                          New Arabidopsis thaliana nucleic acid, for identifying homologous genes, producing compositions that modulate the expression or function of its encoded protein, and mapping functional regions of a protein
                                                                                                                                                                                                                                                                                                                                         Hoffman N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 38; DB 24; Length 465;
Pred. No. 0.22;
0; Mismatches 75; Indels
                                                                                                                                                                                                                                                                                                           Raines TM, L, Woessner G, Allen K, H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 465 BP; 149 A; 101 C; 97 G; 118 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCATTGGTGTAGCCGCAATCTCCATGTCAAACTTCTCC 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 426 CCTCCATCTCTGCGTCGAGGGCCTTGAAGAACTTGTCC 463
                                                                                                                                                                                                                                                                                                           Price JL, Rai
Ledford BL,
, Davis KR, A
                                                                                                                                                                                                                                                                                                         Hamilton CM, Pr
A, Mathew AV, L
r M, Slater T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID 327; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 7.8%;
1 Similarity 52.5%;
83; Conservative
                                                                                                                                                                                                                                                                                                                                           Kricker M,
                                                                                               MATHEW A V.
LEDFORD B L.
WOESSNER J P.
                                                                                                                                                                                                                                                                                                         An Y, Ha
Page A,
HAMILTON C M.
                                                                 RAMEAKA J G.
               PRICE J L.
RAINES T M.
                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-267486/31.
                                                                                                                                                                    GARCIA C A.
                                                                                                                                                                                        KRICKER M.
                                                                                                                                                                                                                         DAVIS K R.
                                                                                                                                                      HAAS W D.
                                                                                                                                                                                                                                                        HOFFMAN N.
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                                                                                                                                                                                                      SLATER T.
                                                                                                                                                                                                                                        ALLEN K.
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                                                                                   PAGE
                                                                                                                                                                                                                                                                                                                                             Sarcia CA,
                                                                                                                                                                                                                                                                                                         Gorlach J,
                                                                                                                                                                                                                                                                                                                                                            Hurban P;
                                                                                                                                                                                                    (SLAT/)
(DAVI/)
(ALLE/)
(HOFF/)
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Best Local
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                                                                                                 MATH/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   396 CCCATCCCTTTCCCGTGTACAAGTAGCTTGCCTCCATCTCTGCGTCGAGGGCCTTGAAGA 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence enocodes a protease which cleaves on the C-terminal side of glutamic acid residues and was isolated from S.fradiae ATCC 14544 genomic DNA. The protease has an optimum pH of 8.2 and a stable pH range at 37 deg.C of 6-9.1 t can be used for the analytical investigation of proteins or to cleave peptide chains at a defined
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTGGCTACGGAAGGACGGGGGGTGCCACCCGGCAGGTGTTGTGGGACTGGCAGTGGCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     336 ACTTGTGGCCCGCCACGCCGGAGAAGACCTGCGTCGTGTCCTGCAGTCGTTGCACACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   714 GCGTGGCGCCCCCCCCCGCGGACCTTGGCGGCGCGCGCTCGGTGGTGACGGTGACGACGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product= glutamic_acid-specific_endopeptidase 435..944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 2064;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C-terminal - is isolated from Streptomyces fradiae ATCC-14544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tsuzuki H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protease which cleaves peptide(s) at glutamic acid residue
                                                                                                                                                                     Streptomyces fradiae glutamic acid-specific protease gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                     endopeptidase; glutamic acid-specific protease; SFase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2064 BP; 270 A; 859 C; 699 G; 236 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 36.2; DB 14;
Pred. No. 1.5;
0; Mismatches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Teraoka H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 5; Page 29-32; 41pp; Japanese.
                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                            Streptomyces fradiae (ATCC 14544).
BP.
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                                                                                              (updated)
(first entry)
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435..1508
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Best Local Similarity 48.33
Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    378.383
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                                                                                                                                                                                                                                                 protein sequencing; ds
                                                                                                                                                                                                                                                                                                                                                                                                /*tag=
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P-PSDB; AAR44216.
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                                                                                           25-MAR-2003
02-JUN-1994
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-35_signal
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which encode human secretory or membrane proteins represented by
AABB8317 - AABB8419. Included in the invention are primers
AABB8317 - AABB8419. Included in the invention are primers
AABB8317 - AABB8419. Included in the invention are primers
CAABB3317 - AAF84285 and AAF86223 - AAF86225 which are used to isolate the cDNA sequences of the invention. The invention also includes methods for the production of antibodies directed against the proteins, and cDNA sequences, which can be used in vaccines. The polynuclectide sequences on the proteins they encode may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate secretory
Crotein/membrane protein expression. The nucleic acids and complementary sequences may also be used as DNA probes in diagnostic assays
(e.g. polymerase chain reactions (PCR)) to detect and quantitate the presence of similar nucleic acid sequences in samples. They may also be used to study the expression and function of secretory proteins/membrane polypeptides and their role in metabolism. The polypeptides may be used as antigens in the production of antibodies against them and in assays to
                                                                       474
                                                                                                   282 GGTGTTGCTGGGCTTCTGGTTCACGTTGCAGGTCTAGGTCTGGGTGCCCAGGCTGCTGCT 223
agents to down regulate expression and activity. The antibodies may also be used as diagnostic agents for detecting the presence of the polypeptides in samples (e.g. by enzyme linked immunosorbant assay (ELISA). Examples of diseases which may be treated include rheumatoid arthritis and diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               identify modulators (agonists and antagonists) of expression and activity. The antibodies and antagonists may also be used as therapeutic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids encoding secretory proteins/membrane proteins, useful in
                                                                         CAAGTAGCTTGCCTCCATCTCTGCGTCGAGGGCCTTGAAGAACTTGTCCATGTCGAAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention relates to nucleic acid sequences AAF93744 - AAF93916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human cDNA encoding a membrane or secretory protein clone PSEC0236.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; secretory protein; membrane protein; vaccine; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hayashi K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene therapy or as candidate target molecules in drug development
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isogai T, Nishikawa T, Kawai Y, Sugiyama T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID 267; 609pp + CD ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rheumatoid arthritis; diabetes; ss.
                                                                                                                                                                                                                                                                                                                                            AAF93877 standard; cDNA; 1906 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-JUL-1999; 99JP-0194179.
11-JAN-2000; 2000JP-0118775.
02-MAY-2000; 2000JP-0183766.
                                                                                                                                                                                                                                                                                                                                                                                                                                        23-MAY-2001 (first entry)
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                                                                                                                                                                     475 GGCCGTGG 482
                                                                                                                                                                                                                     222 GGGCACGG 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-093989/11.
P-PSDB; AAB88450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-JAN-2001.
                                                                                                                                                                                                                                                                                                                                                                                        AAF93877;
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                                                                                                                                                                                                                                                                                                                        AAF93877,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           355 GGAGAAGACCTGCGTGCTGCCTGCAGTCGTTGCACACGACCCATCCCTTTCCCGTGTA 414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This DNA sequence codes for an immunoglobulin (Ig) C-gamma-3 region (see AAW37345). The invention provides a method for the production of tumour-specific Ig derived from a D-cell lymphoma patient. In the movel method, expression plasmids containing the patient's VH region(s) joined to either a C-gamma-3 or C-gamma-4 patient's VL region(s) joined to either a C-gamma-3 or C-gamma-4 patient's VL region(s) joined to either a C-kappa (see AAT97190) of C-lambda-2 (see AAT97191) sequence are corransfected along with a BW5147.G.1.4), and transfected call line (e.g. BW5147.G.1.4), and transfected calls are then subjected to selection and amplification. The method permits the production of a multivalent vaccine which reflects the degree of somatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Multivalent vaccine to treat B cell lymphoma or leukaemia - comprises at least 2 different recombinant variable regions of immunoglobulin molecules derived from B cell lymphoma cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.4%; Score 36; DB 18; Length 1147;
49.5%; Pred. No. 1.3;
tive 0; Mismatches 95; Indels (
                                                                                                                                                                                                                                                                                                                                       Vaccine; B-cell malignancy; lymphoma; leukaemia; tumour; gene amplification; immunotherapy; therapy; immunoglobulin; C-gamma-3; constant region; ds.
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Example 10; Page 121-123; 177pp; English
                                                                                                                                                                                                                                                                                            Immunoglobulin C-gamma-3 region DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers 7..1140
                                                                                                                            188/c
AAT97188 standard; DNA; 1147 BP
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96US-0644664.
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                                                                                                                                                                                                                                            (first entry)
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les 93; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1997-549743/50.
P-PSDB; AAW37345.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9741244-A1
                                                                                                                                                                                                                                            11-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-APR-1997;
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                                                                                                                                                                                            AAT97188;
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Matches
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Gaps

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0; Mismatches 110;

DB 22; Length 25360; 4.9; Indels

Score 36; Pred. No. 4

7.48;

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This invention describes a novel method nucleic acid (I) and its encoded polyaeptide (II) containing at least one region that encodes an enzymatic activity involved in biosynthesis of spinosyns. (I) are used (i) to identify, inactivate or modulate genes involved in the biosynthesis of identify, inactivate or modulate genes involved in the biosynthesis of adding forosamine or trimethylrhamnose to a spinosyn or polyketide allorance and (IV) for recombinant production of the corresponding enzymes, which are used for production of (II), their precursors or derivatives, including production of (II), their precursors or derivatives, including production of transgenic plants that express (II) and thus have increased resistance to insects. (I) are also useful as markers for sequencing of the Saccharopolyspora spinosa genome. (II) are macrolides with insecticidal, but not antibacterial, activity, and can also be used to raise specific antibodies, useful for identifying expression clones in a gene bank. Cells transformed with (I) may produce (II) at significantly increased levels or produce new derivatives of genome which contains the coding regions for proteins involved in the contains the coding regions for proteins involved in consemine, trimethylrhamnose and polyketide synthase biosynthesis.
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                                                                                                                         307 GCAGGTGTTGTGGGACTGGCAGTGGCACTTGTGGCCCGCCACGCCGGAGAAGACCTG 366
                                                                                                                                                New nucleic acid encoding enzymes for spinosyn biosynthesis, useful for recombinant production of insecticidal spinosyns and their derivatives
                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polyketide synthase; biosynthesis;
transgenic plant; insect resistance;
                                                                                           ö
                                                        Length 1906;
                                                                                         35; Indels
                  Sequence 1906 BP; 338 A; 671 C; 578 G; 319 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Salas JA;
                                                      22;
                                                                                                                                                                                                367 CGTCGTGTCCTGCAGTCGTTGCACACGACCC 398
                                                                                                                                                                                                                     DB
                                                                                        0; Mismatches
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                                                    Score 36;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   S. spinosa DNA fragment SEQ ID 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Forosamine; trimethylrhamnose;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      spinosyn; polyketide aglycone; macrolide; insecticidal; ds.
                                                                                                                                                                                                                                                                                                       AAF88314/C
ID AAF88314 standard; DNA; 25360
                                                      7.48;
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                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharopolyspora spinosa.
                                                                                        57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eberz G, Moehrle V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-267102/28.
                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (FARB ) BAYER AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DE19957268-A1
                                                                                                                                                                                                                                                                                                                                                                                                 28-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                                AAF88314;
                                                                                         Matches
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Sequence 25360 BP; 3832 A; 9143 C; 8354 G; 4031 T; 0 other;

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12675 ATCGCGACGCGCCCAGCGGCGGGCAGGGCCACCCGGTAGAAGATGCCC 12616
                                                                                                                                                                                                                                                               394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention describes a novel method nucleic acid (1) and its encoded polypeptide (II) containing at least one region that encodes an enzymatic activity involved in biosynthesis of spinosyns. (I) are used (i) to identify, inactivate or modulate genes involved in the biosynthesis of (II); (ii) to generate a library of polyketide synthases; (iii) for
                                                                                    275 GGTGGCTACGGAAGGACGGGGGGGGGTGCCACCCGGCAGGTGTTGTGGGACTGGCAGTGGCAG 334
                                                                                                                                                                                                                                       454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     adding forosamine or trimethylrhamose to a spinosyn or polyketide aglycone; and (iv) for recombinant production of the corresponding enzymes, which are used for production of (II), their precursors or derivatives, including production of transgenic plants that express (II) and thus have increased resistance to insects. (I) are also useful as markers for sequencing of the Saccharopolyspora spinosa genome. (II) are macrolides with insecticidal, but not antibacterial, activity, and can also be used to raise specific antibodies, useful for identifying expression clones in a gene bank. Cells transformed with (I) may produce (II) at significantly increased levels or produce new derivatives of (II). This sequence represents a genomic DNA fragment of the S. spinosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid encoding enzymes for spinosyn biosynthesis, useful for recombinant production of insecticidal spinosyns and their derivatives
                                                                                                                                                              335 CACTTGTGGCCCGCCACGCCGGAGAGACCTGCGTGTCGTGTCCTGCAGTCGTTGCACACG
                                                                                                                                                                                                                                       395 ACCCATCCCTTTCCCGTGTACAAGTAGCTTGCCTCCATCTCTGCGTCGAGGGCCTTGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polyketide synthase; biosynthesis;
transgenic plant; insect resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Salas JA;
                                                                                                                                                                                                                                                                                                                                     12555 AACTGGCGCATGATGAAGATCGCCAGCACACA 12524
                                                                                                                                                                                                                                                                                                                  455 AACTTGTCCATGTCGAAGATGGGCGTGGCGCA 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Velten R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 7; Page 92-102; 354pp; German.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               AAF88317 standard; DNA; 29736 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Forosamine; trimethylrhamnose; spinosyn; polyketide aglycone; macrolide; insecticidal; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S. spinosa DNA fragment SEQ ID
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Query Match
Best Local Similarity 48.19
Watches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharopolyspora spinosa.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-267102/28
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P-PSDB; AAW15412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-APR-1997.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAT64548;
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AAT64548/c
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                                                                                                                                                                                                                                                                17051 ATCGCGACGCCCCAGCGCGGGCCGGGACAGCGGCCACCCGGTAGAAGATGCCC 16992
                                                                                                                                                                                                                                                                                                                                                  16991 GCTCGTCCGAGGCCGTCCATCCGCGGGCCTCCTCCAGCTCCGACGGCAGGGGGGATGAAG 16932
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequences AAS63224-AAS63305 represent cDNA encoding and PCR primers used to amplify cDNA encoding proteins which can be used in the synthesis of chimeric proteins comprising a DNA mutation-binding protein, a linker and a nuclease, by recombinant technology. The chimeric proteins are useful for detection, quantification and mapping of DNA sequence variations
                                                                                                                                                                                                                                                                                                                  454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA damage; human xeroderma pigmentosum complementation group; XPF; XPA; XPC; XPE; ERCC4; human MutS homologue 2; hMSH2; MutS; Nuc; MutY; Fpg; ss; Fapy-DNA glycosylase; uracil DNA glycosylase; uracil DNA glycosylase; uracil CNT A; A/G-specific adenine glycosylase; synthetic T4 endonuclease V; T4 endo V; thymine DNA-glycosylase; Uvr B; Uvr C; nth gene; nfo gene; exonuclease;
                                                                                                                                                                275 GGTGGCTACGGAAGGACGGGGGTGCCACCCGGCAGGTGTTGTGGGGACTGGCAGTGGCAG 334
                                                                                                                                                                                                                                       335 CACTIGIGGCCCGCCACGCCGGAGAAGACCIGCGICGIGGTCCCIGCAGACGTTGCACACG 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Recombinant chimeric protein, useful for detecting and quantifying DNA mutations, e.g. in disease diagnosis, comprises mutation-binding protein and nuclease -
                                                                                                                                                                                                                                                                                                            ACCCATCCCTTTCCCGTGTACAAGTAGCTTGCCTCCATCTCTGCGTCGAGGGCCTTGAAG
                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA encoding Thermus thermophilus MutS DNA mutation binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mutation-binding protein; nuclease; DNA mismatch; cancer; PCR
proteins involved in
                                                                                                                            ö
                                                                                          Length 29736;
                                                                                        Query Match 7.4%; Score 36; DB 22; Length 29
Best Local Similarity 48.1%; Pred. No. 5.3;
Matches 102; Conservative 0; Mismatches 110; Indels
                                                   Sequence 29736 BP; 4401 A; 10346 C; 10080 G; 4909 T;
                                                                                                                                                                                                                                                                                                                                                                                                          16931 AACTGGCGCATGATGAAGATCGCCAGCACACA 16900
genome which contains the coding regions for processamine and trimethylrhamnose biosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                     455 AACTIGICCATGICGAAGAIGGGCGIGGCGCA 486
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAS63231/c
ID AAS63231 standard; cDNA; 3283
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2000US-0650855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mc Cutchen-maloney SL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thermus thermophilus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-656920/75.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  endonuclease
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                                                                                                                                                                                                                                                                                                              395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   304 CCGGCAGGTGTTGTGGGACTGGCAGTGGCAGCACTTGTGGCCCGCCACGCCGGAGAAGAC 363
including mutations, for example, caused by damage and mismatches. The proteins are able to bind to the site of the DNA mutation and cut it out of the molecule. This is useful for early diagnosis of cancer and other diseases. The proteins used in the invention include human XPF (or ERCC4), human xeroderma pigmanchosum complementation groups A, C and E (XPA, XPC and XPE), human MutS homologue 2 (hMSH2), Serratia marcescens nuclease (Nuc), Thermus thermophilus MutS, Escherichia coli Rapy-DNA glycosylase (Fpg), uracil DNA glycosylase (unty), A/G-specific adenine glycosylase (MutY), synthetic 74 endonucleases V (T4 endo V), thymine DNA-glycosylase (TDG), E. coli Uvr A, B and C, and E. coli endonucleases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                364 CTGCGTCGTGTCCCTGCAGTCGTTGCACACGACCCATCCCTTTCCCGTGTACAAGTAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 35.8; DB 22; Length 3283;
Pred. No. 2.4;
0; Mismatches 72; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glutamate dehydrogenase; NADP-GDH; alga; nitrogen metabolism;
                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3283 BP; 514 A; 1093 C; 1139 G; 537 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NADP-specific glutamate dehydrogenase beta subunit cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1966 GCCCGTCCTCTCTCTCCGGGCCTCGAGG 1936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             424 TGCCTCCATCTCTGCGTCGAGGGCCTTGAAG 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chlorella sorokiniana strain UTEX 1230.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.3%;
52.3%;
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Best Local Similarity 52.3
Matches 79; Conservative
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4..1431
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                                                                                                                                                                                                                                                                                                                                     1238 AGGCCGCTGACCGCCACGCCGCCGCGTTGGCCGCCTTGCCGGGGCAGTAGATGATGCCG 1179
                                                                                                                                                                                                                                                                                                                                                                                        1178 GCCTTGTTGTACTTGTGGATGCCTTCGTTGGTGGAGGCCATGTTGGCGCCCTCCACCACG 1119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                1118 TACTGGCAGCCGTGCTTGATCAGCAGCTCGGCGTCGTGCTCATCGATCTCGTTCTGGGTG 1059
                                                                                                                                                                                                                                                                                                         287 AGGACGGGGGGTGCCACCCGGCAGGTGTTGTGGGACTGGCAGTGGCAGCACTTGTGGCCC 346
                                                                                                                                                                                                                                                                                                                                                                347 GCCACGCGGAGAAGACCTGCGTCGTGTCCCTGCAGTCGTTGCACACGACCCATCCCTTT 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product "Mature NADP-specific glutamate dehydrogenase beta subunit"
                                                                                                                                                                                                                                                                                                                                                                                                                      407 CCCGTGTACAAGTAGCTTGCCTCCATCTCTGCGTCGAGGGCCTTGAAGAACTTGTCCCATG
          (AAW15411) and beta mature subunits (AAW15412) of ammonium inducible, chloroplast-localised NADP-specific glutamate dehydrogenase (NADP-CDF) wheremeric isoenzymes of Chlorellas sorokiniana. They were obtd. by removal of the chloroplast targeting signal from fulllength cDNA clones (see also AAT64542-43) by PCR mutagenesis. The N metabolism of plant cells can be modulated (pref. increasing the assimilation of inorganic N into organic N) by transforming them with nucleotide sequences encoding the alpha and/or beta mature show improved properties, e.g. increased crop yield and improved stress tolerance. Heterohexamers having alpha and beta subunits can be expressed that have higher aminating:deaminating activity ratios (i.e. higher capacity for glutamate synthesis) than
                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alga; nitrogen metabolism; plant; ammonium assimilation; transgenic; ammonia toxicity tolerance; osmotic stress tolerance; gene; ss.
clones (AAT64547 and AAT64548) respectively code for the alpha
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                                                                                                                                                                                                                                                   Score 35.6; DB 18; Length 1473;
Pred. No. 2;
0; Mismatches 94; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA encoding mature NADP-glutamate dehydrogenase beta subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NADP-specific glutamate dehydrogenase; NADP-GDH; beta subunit;
                                                                                                                                                                                                                          Sequence 1473 BP; 297 A; 486 C; 470 G; 220 T; 0 other;
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ABK51026 standard; cDNA; 1473
                                                                                                                                                                                                                                                   7.38;
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                                                                                                                                                                                                                                                                  1 Similarity 49,5
92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4..1434
/*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chlorella sorokiniana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1058 GCGCAG 1053
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                                                                                                                                                                                                homohexamers.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 406
                                                                                                                                                                                                                                                                                                 The invention relates to a method of modulating nitrogen metabolism in plant cells, comprising transforming a plant cell with a polynucleotide encoding a polypeptide having glutamate dehydrogenase activity, and culturing the cell to produce descendant cells which express the polypeptide. The method is used to provide plants with increased yield, improved ammonium assimilation properties, increased tolerance to ammonia toxicity, improved osmotic stress tolerance and improved composition. The present sequence represents the coding sequence of mature Chlorella sorokiniana NADP-glutamate dehydrogenase beta subunit.
                                                                                  Transforming a plant with a polynucleotide encoding a polypeptide with glutamate dehydrogenase activity provides a plant with modulated nitrogen metabolism useful to increase yield and ammonium and osmotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 347 GCCACGCCGGAGAAGACCTGCGTCGTGCTCCTGCAGTCGTTGCACGACCCATCCCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          407 CCCGTGTACAAGTAGCTTGCCTCCATCTCTGCGTCGAGGGCCTTGAAGAACTTGTCCATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 35.6; DB Pred. No. 2; 0; Mismatches
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                                                                                                                                                                                                                                              Example 2; Page 31-32; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                used in the method of the invention.
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Best Local Similarity 49.55
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WPI; 2002-499691/53.
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